OIPE

#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/987,701

DATE: 12/06/2001
TIME: 15:06:11

Input Set : A:\es.txt
Output Set: N:\CRF3\12062001\I987701.raw

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 3 <110> APPLICANT: BASCH, Ross S.
 4        ZHANG, Xin-Min
 6 <120> TITLE OF INVENTION: PROTEIN THAT MODULATES THE STABILITY OF TRANSCRIPTIONAL
REGULATORY
 7        COMPLEXES REGULATING NUCLEAR HORMONE RECEPTOR ACTIVITY, DNA ENCODING SAME, AND
 8        ANTIBODIES THERETO
10 <130> FILE REFERENCE: BASCH=1A
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/987,701
13 <141> CURRENT FILING DATE: 2001-11-15
15 <150> PRIOR APPLICATION NUMBER: 60/248,191
16 <151> PRIOR FILING DATE: 2000-11-15
18 <160> NUMBER OF SEQ ID NOS: 17
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3885
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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29 <222> LOCATION: (161)..(1705)
30 <223> OTHER INFORMATION:
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (2487)..(2487)
36 <223> OTHER INFORMATION: n is a, c, g or t.
39 <220> FEATURE:
40 <221> NAME/KEY: misc_feature
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42 <223> OTHER INFORMATION: n is a, c, g or t.
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48 attggcggtg accggatatt cagttgcaca tccccacatc aatgcactgc caatgggtta      120
50 tatcctgtgt tgtgacctca tggtttaagt gggaataaag atg agt ata agc agt      175
51                                                 Met Ser Ile Ser Ser
52                                                 1               5
54 gat gag gtc aac ttc ttg gta tat aga tac ttg caa gag tca gga ttt      223
55 Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu Gln Glu Ser Gly Phe
56                 10                  15                  20
58 tct cat tca gca ttt acc ttt ggt ata aaa agc cat atc agt cag tcc      271
59 Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser
60                 25                  30                  35
62 aat ata aat ggt gcc ctc gtc cca ccc gct gca ttg att tct atc atc      319
63 Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile
64         40                  45                  50
66 cag aaa ggt cta cag tat gta gaa gca gaa gtt agt att aat gag gat      367
67 Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val Ser Ile Asn Glu Asp
68     55                  60                  65
70 ggt acc ttg ttt gat ggt cga cca ata gag tct ctg tcc ctg ata gat      415
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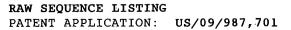
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71 Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser Leu Ser Leu Ile Asp
72 70              75              80              85
74 gcc gta atg cct gat gta gta caa aca aga caa caa gct tat aga gat      463
75 Ala Val Met Pro Asp Val Val Gln Thr Arg Gln Gln Ala Tyr Arg Asp
76              90              95              ·100
78 aag ctt gca cag caa cag gca gca gct gct gca gct gcc gca gct gca      511
79 Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
80          105             110             ·   115
82 gcc agc caa caa gga tct gca aaa aat gga gaa aac aca gca aat ggg      559
83 Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu Asn Thr Ala Asn Gly
84          120             125             130
86 gag gag aat gga gca cat act ata gca aat aat cat act gat atg atg      607
87 Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn His Thr Asp Met Met
88      135             140             145
90 gaa gtg gat ggg gat gtt gaa atc cct cct aat aaa gct gtt gtg ttg      655
91 Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn Lys Ala Val Val Leu
92 150             155             160             165
94 cgg ggc cat gaa tct gaa gtt ttt atc tgt gcc tgg aac cct gtt agt      703
95 Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala Trp Asn Pro Val Ser
96              170             175             180
98 gat ctc cta gca tca ggg tct gga gac tca aca gca aga ata tgg aat      751
99 Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr Ala Arg Ile Trp Asn
100             185             190             195
102 ctt agt gag aac agc acc agt ggc tct aca cag tta gta ctt aga cat     799
103 Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln Leu Val Leu Arg His
104         200             205             210
106 tgt ata cga gaa gga ggg caa gat gtt ccg agc aac aag gat gtc aca     847
107 Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser Asn Lys Asp Val Thr
108     215             220             225
110 tct cta gat tgg aat agt gaa ggt aca ctt cta gca act ggt tcc tat     895
111 Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu Ala Thr Gly Ser Tyr
112 230             235             240             245
114 gat ggg ttt gcc aga ata tgg act aaa gat ggt aac ctt gct agc acc     943
115 Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly Asn Leu Ala Ser Thr
116         250             ·255            260
118 tta ggg cag cat aaa ggc cct ata ttt gca tta aaa tgg aat aag aaa     991
119 Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu Lys Trp Asn Lys Lys
120         265             270             275
122 gga aat ttc atc cta agt gct gga gta gac aag act aca att att tgg     1039
123 Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys Thr Thr Ile Ile Trp
124         280             285             290
126 gac gca cat act ggt gaa gcc aag caa cag ttt cct ttt cat tca gca     1087
127 Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe Pro Phe His Ser Ala
128     295             300             .305
130 cca gca ttg gat gtt gat tgg cag agc aac aac acc ttt gct tct tgt     1135
131 Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn Thr Phe Ala Ser Cys
132 310             315             320             325
134 agt aca gat atg tgc att cat gtc tgt aaa tta gga caa gac aga cct     1183
135 Ser Thr Asp Met Cys Ile His Val Cys Lys Leu Gly Gln Asp Arg Pro
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136                 330                 335                 340
138 att aaa aca ttc caa gga cat acg aat gaa gta aat gct atc aaa tgg     1231
139 Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val Asn Ala Ile Lys Trp
140         345                 350                 355
142 gac cca act ggc aat ctc ttg gcc tcc tgt tct gac gac atg act tta     1279
143 Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser Asp Asp Met Thr Leu
144         360                 365                 370
146 aag ata tgg agt atg aaa caa gac aat tgt gtc cat gat ttg cag caa     1327
147 Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Gln
148     375                 380                 385
150 cat aat aaa gaa att tat act atc aaa tgg agt cca aca gga cca ggg     1375
151 His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser Pro Thr Gly Pro Gly
152 390                 395                 400                 405
154 act aat aat cca aat gcc aac ctt atg tta gca agt gca tcc ttt gat     1423
155 Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala Ser Ala Ser Phe Asp
156                 410                 415                 420
158 tct act gtt agg tta tgg gat gta gac cga ggg ata tgc atc cat acc     1471
159 Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr
160         425                 430                 435
162 ttg aca aaa cac caa gag cct gtg tac agt gta gct ttc agt cct gat     1519
163 Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val Ala Phe Ser Pro Asp
164         440                 445                 450
166 ggc agg tat ctg gca agt ggt tct ttt gac aaa tgt gta cac atc tgg     1567
167 Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys Cys Val His Ile Trp
168     455                 460                 465
170 aac acg cag aca ggt gct cta gtt cac agc tat agg gga aca ggt gga     1615
171 Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr Arg Gly Thr Gly Gly
172 470                 475                 480                 485
174 ata ttt gaa gtt tgc tgg aat gca gca gga gac aaa gtt gga gcc agt     1663
175 Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp Lys Val Gly Ala Ser
176                 490                 495                 500
178 gca tca gat ggt tca gtt tgt gta tta gac ctt cgg aaa tag     1705
179 Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu Arg Lys
180         505                 510
182 cgctactagt tggaagccat ggaccgacta tgaatgtgta catagccaaa atgagtgtcc     1765
184 ctgacccatg taatgttata gtcccacttg aaccatggcc agtccaatac agccaaatct     1825
186 aaaagaaata tatacataca gtgtatataa acaaaattac accctgaaga tgacagagtt     1885
188 ttgtcacagc ttgtgaattc tgttcaccaa gtgctggaat ctaatctgct gtgcccctaa     1945
190 aatagcattt agaagttttg gatatgaaaa acagaagaga gaaaatatac attataaaag     2005
192 cagtacatac atgtaccagt ttttggatac taaatgacag ccttgtttct cccctttgaa     2065
194 tcagcagaca ccatggatta tattcttttt ttcccttcag tagtgagcag tttgtatgta     2125
196 cagagaaaat ggacttacaa aaacttgcag cagtagtttg ttcttgcttt aaaatttcgt     2185
198 ttttggttta gattatggat gcatgaagta agggagtgaa tcagtttctt gtttatattt     2245
200 ttttcacctt ttaaacaaaa aattctttaa aatattttaa tgcattcttt tgaagaggta     2305
202 gatgtttggt acattttatg gctcccagag catatattca gttggtgcat gttgtggaag     2365
204 ggggaattgg aaattaaatg gaaaacctat gactttggtc ctgtcaatct gtaagacaca     2425
206 tcagtaaaaa ggtattatgc tctgttggtt ttgttttttt gttttgcttt ttttttttt     2485
208 tnctttttg ttttttggtg atgtggctta aatgcaatag tttctttttt gggacatatt     2545
210 tctgccaatt aaagactaga agggcacaac tttttttta attaccatag agaagataca     2605
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214 ttgtgaaaag gagcaacgta gttttgggtt ttttgttgtt tgtttgtttt gctttgtttt 2725
216 ttaagagatt aaaatgtttc tggataagga ttagcttctc gaagtgtcca tcattctgtg 2785
218 tanaagctta aatatgtaat gtaaccaaac tccagtatta aaaatctctc atgttgtttt 2845
220 ctttatacaa agcaagataa cggcatataa cactgccatt acatggcaaa atgtttgcta 2905
222 ccttagttta aaaaacaatc tcaaacaaaa gacttgcttc aaggtgtttt taaatagcag 2965
224 tgattcagaa ttttttttaa tgaaagtata attgcactaa ccttcttcct gctgctctga 3025
226 ttctgcattt gtggtacttg tgactacgtt ttttcaaata tagatagatt taagctgcta 3085
228 attttttttt ttttagtaat cactactata tcatgtcttt tactctgttt ataatatcaa 3145
230 gtatttctt aaagatatag atattaaacc ttgtgctcat gcaacttaga gtaacatata 3205
232 cagacaaatg attgcatgag gccatgttta tatgtgtgac taataaggct tgtcatgatt 3265
234 aacataatcc aggtatgtca tttctgaaga gaatagtcat caaatttata tctcgaagat 3325
236 tttaattaag ggaattgctt attgtttgag cttagcaaat taataacact atttctgtca 3385
238 ctaattattt tgaggccttt tagtactaaa attttaacct gtgttctaag tagaaactga 3445
240 tttaacccaa gtaatgcagc tttgattgat ttcagcattc gttgctttgc tatttttaca 3505
242 aaacagcatt gattgaagca agttttggtt ttactaaggt agggtagcat ttgctattgg 3565
244 taaagagaat aaatacactt aatttcacaa tacattgtta tatgtacccc agttgttgtt 3625
246 agtgggggact atgatactgt aataatattt ttaaaaattt acatcaagag aggcagtcat 3685
248 tcacgatggt tttgtgccag ctcttttttag ggttttggat cacattagag atatttagaa 3745
250 catattaccc tgtgacttac gtaggaaacc taatatgctg agtatctggc acttgaattc 3805
252 ctgctttttat tgctggaggt ccacatgtgt ggttgacctc tgttattgtt taaaaaaaaa 3865
254 aaaaaaaaaa aaaaaaaaaa 3885
257 <210> SEQ ID NO: 2
258 <211> LENGTH: 514
259 <212> TYPE: PRT
260 <213> ORGANISM: Homo sapiens
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263 <400> SEQUENCE: 2
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270             20                  25                  30
273 His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
274         35                  40                  45
277 Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
278     50                  55                  60
281 Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
282 65                  70                  75                  80
285 Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
286             85                  90                  95
289 Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala
290             100                 105                 110
293 Ala Ala Ala Ala Ala Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu
294         115                 120                 125
297 Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
298     130                 135                 140
301 His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn
302 145                 150                 155                 160
305 Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala
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306                   165                 170                 175
309 Trp Asn Pro Val Ser Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr
310                   180                 185                 190
313 Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln
314         195                 200                 205
317 Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser
318         210                 215                 220
321 Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu
322 225                 230                 235                 240
325 Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly
326             245                 250                 255
329 Asn Leu Ala Ser Thr Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu
330             260                 265                 270
333 Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys
334         275                 280                 285
337 Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe
338         290                 295                 300
341 Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn
342 305                 310                 315                 320
345 Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu
346             325                 330                 335
349 Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val
350         340                 345                 350
353 Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser
354         355                 360                 365
357 Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val
358         370                 375                 380
361 His Asp Leu Gln Gln His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser
362 385                 390                 395                 400
365 Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala
366             405                 410                 415
369 Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly
370         420                 425                 430
373 Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val
374         435                 440                 445
377 Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys
378     450                 455                 460
381 Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr
382 465                 470                 475                 480
385 Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp
386             485                 490                 495
389 Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu
390             500                 505                 510
393 Arg Lys
397 <210> SEQ ID NO: 3
398 <211> LENGTH: 2078
399 <212> TYPE: DNA
400 <213> ORGANISM: Homo sapiens
402 <220> FEATURE:
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/987,701**

DATE: 12/06/2001
TIME: 15:06:12

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\12062001\I987701.raw**

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L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:263 M:283 W: Missing Blank Line separator, <400> field identifier